Attorney Docket No. 3108.1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

In re application of:

Mittmann et al.

Serial No: 09/827,383

Filing Date: April 4, 2001

Title: TAG NUCLEIC ACIDS AND PROBE ARRAYS

Examiner: J. Fredman

Group Art Unit: 1637

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Commissioner for Patents
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REPLY BRIEF

Sir:

Appellants submit this Reply Brief in response to the Examiner's Answer mailed July 28, 2005.

The Appeal Brief pointed out that the claimed invention has a utility that is substantial and specific and meets the requirements for utility as set forth in Brenner v. Manson, 383 U.S. 519, 148 U.S.P.Q. 689 (1966) and in the Utility Examination Guidelines issued by the PTO and incorporated into the Manual of Patent Examining Procedure ("MPEP"). See MPEP § 2107.01. The claims are drawn to sets of at least 1,000 tag sequences selected from a list of 2,000 DNA sequences provided in the sequence listing. The sequences are all 20 bases in length and are artificial sequences that were selected from a list of randomly generated combinations of A, C, G and T. The

sequences do not occur in nature. The 2,000 sequences were selected to have closely matched hybridization performance. The set of sequences was further filtered to remove sequences that would cross hybridize to other sequences in the set or to known genomic sequences. The resulting set of sequences can be used as a group to independently and uniquely mark 2,000 different items and all tags in the set can be uniquely identified in a single hybridization experiment to an array of complementary tag probes. Affymetrix sells a commercial product, the GENECHIP GENFLEX tag array that is an embodiment of the claimed invention.

The Examiner's comment in section (8) of the Answer, "Grounds of Rejection", appears to be identical to the rejection in the final office action of January 31, 2005, which was addressed in the Appeal Brief. Appellants believe that the arguments provided in the Appeal Brief support a conclusion that the claimed invention has patentable utility. Accordingly, no further response is necessary.

In section (9) of the Answer, "Response to Argument", the Examiner addresses some but not all of Appellants' remarks in the Appeal Brief. In the Examiner's Answer there is no discussion of Appellants' assertion that the patentability of the claims is consistent with prior practice of the U.S. Patent Office. Appellants pointed out and provided issued claims from two separate U.S. Patents that claim sets of tag nucleic acids. (See the Appeal Brief at pages 12-13).

On page 11 and 12 of the Answer, the Examiner has included a discussion of some recent Board of Patent Appeals and Interference in support of the conclusion that "Using a sequence on a microarray does not provide specific utility for the sequences on the microarray." (Answer at 11). Appellants do not dispute this point and, as the

Examiner points out, this is entirely consistent with the position taken by Affymetrix in the Brief for Amicus Curiae Affymetrix, Inc. filed in support of the Board of Patent Appeals and Interference (BPAI) decision in In re Fisher (Amicus Brief).

As noted by the Examiner, Ex parte Turner et al. App. No. 2004-1843 (Bd. Pat. App. Int. Oct. 22, 2004), provides a discussion of whether simply attaching a sequence to an array should be sufficient for patentability. In Turner, the claimed subject matter was a nucleic acid sequence encoding a naturally occurring protein with no known function and the Appellant argued that the claimed polynucleotide had utility as a probe on a DNA chip. The Board disagreed stating:

> Assuming arguendo that a generic DNA chip—one comprising a collection of uncharacterized or semi-characterized gene fragments—would provide a useful tool for, e.g., drug discovery, it does not follow that each one of the polynucleotides represented in the DNA chip individually has patentable utility. Although each polynucleotide in the DNA chip contributes to the data generated by the DNA chip overall, the contribution of a single polynucleotide—its data point—is only a tiny contribution to the overall picture. Id., slip op. at 18.

The Board further concluded that, "Providing a single data point among thousands, even if the thousands of data points collectively are useful, does not meet [the Brenner Court] standard (emphasis in original)." Id. It is clear from Turner that a single probe for an uncharacterized or semi-characterized gene would not meet the standard for utility, whether on an array or not, but Turner does not address the minimum number of data points that would be required to meet the standard and the minimum level of characterization necessary.

Unlike the Appellant in both Fisher and Turner Appellants are not claiming a single EST with no known biological function. The claimed tag sequences are similar to

ESTs only in that they are both nucleic acids. While ESTs are derived from genomic sequence and presumably correspond to a gene that has a biological function, the tag sequences are selected to not be genomic sequence and should not have a biological function. Appellants have also not asserted that the utility of the claimed sets of tag sequences is dependent on attachment to a solid support or that simply attaching a sequence with no known function, either biological or otherwise, to a microarray provides a specific and substantial utility for that sequence. In fact, independent claims 1 and 2 do not require that the tag sequences be attached to a solid support.

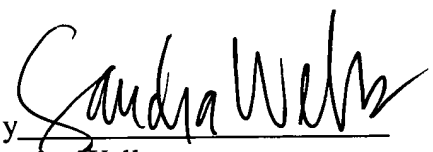
On page 13 of the Answer, the Examiner indicates that, "If the current Appellant is correct, then any nucleic acid whatsoever has utility as a tag, irrespective of whether there is any specific or substantial utility known for the sequence." The Examiner further concludes that, "Appellant's argument would lead to the inevitable conclusion that every biological molecule has utility as a tag on a microarray." Appellants disagree. The Examiner appears to base this conclusion on the assumption that any molecule that has a partner that it interacts specifically with can be used as a tag with the same utility as the claimed set of tags. The Examiner suggests that any genomic fragment or any protein would have the same utility as the claimed sets of tags because the molecule interacts specifically with a complement or a protein. The tags in the claimed set of tags have the characteristic that they interact specifically with a complement, but they have been further selected to share additional common characteristics that make them particularly well suited as tags, for example, they are not naturally occurring biological molecules so they would not be expected to have a function in a cell. Tagging a molecule of interest with a protein that has its own biological function or a molecule that is present in nature

is likely to interfere with the function of the protein as a tag. Larger molecules such as proteins and gene sequences are also more likely to interact specifically or non-specifically with other molecules that may be present in the system being analyzed, making them less suitable to function as tags. Appellants is not suggesting that there are no other sets of molecules that could be used as tags, but there are a limited number of combinations of 1,000 or more molecules that would have the same utility as the claimed sets of tags. Certainly the utility of the claimed tag sets is not applicable to the broad class of all biological molecules.

For these reasons, as well as those submitted in the Appeal Brief, Appellants respectfully submit that rejection of pending Claims 1, 2, 7 and 15-19 is improper. Accordingly, Appellants request that the rejection of Claims 1, 2, 7 and 15-19 be reversed.

Respectfully submitted,

Date: September 28, 2005

By 
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